

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gary S. Gray et al.
- (ii) TITLE OF INVENTION: CTLA-4-C/4 Fusion Proteins (As Amended)
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet available
 - (B) FILING DATE: December 20, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/227,595
 - (B) FILING DATE: January 8, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Amy E. Mandragouras
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPN-001CN
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10027075.122001

CATTCTAGAA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC

43

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCAGGCTG GGCCACGTGC ATTGCGGAGT GGACACCTGT GGAGAG

46

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCCACAG GTGTCCACTC CGCAATGCAC GTGGCCCAGC CTGCTG

46

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTGTGTGGA ATTCTCATTG CTGATCAGAA TCTGGGCACG GTTCTG

46

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTTTAAG CTITTTCTCTG ATCAGGAGCC CAAATCTTCT GACAAAAC TC ACACATCTCC 60

ACCGTCTCCA GGTAAGCC 78

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCATTTTC CTGATCAGGA GTCCAAATAT GGTCCCCAC CCCATCATCC CCAGGTAAGC 60

CAACCC 66

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10027075.122001

GCAGAGGAAT TCGAGCTCGG TACCCGGGGA TCCCCAGTGT GGGGACAGTG GGACCCGCTC 60
TGCCTCCC 68

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTTTGGG GGAAGAGGA AGACTGACGG TGCCCCCTCG GCTTCAGGTG CTGAGGAAG 59

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCTCTTCC TCAGCACCTG AAGCCGAGGG GGCACCGTCA GTCTTCTCTT TCCCC 56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCAGCTGAC CTCAGGGGTC CGGGAGATCA TGAGAGTGTC CTTGGGTTTT GGGGGGAACA 60

GGAAGACTGA TGGTCCCCC TCGAAGTCAG GTGCTGAGG 99

(2) INFORMATION FOR SEQ ID NO:12:

10027075.122001

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCAGCACC TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCA AAACCCAAGG 60
ACACTCTCAT GATCTCCCG ACCCCTGAGG TCACGTGCG 99

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATTGCTTA CCTGACAAG CTGAGATCA CAGTTCTCTC TAC 43

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGTGGACA CCTGTGGAGA G 21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10027075.122001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCCACAGGT GTCCACTCCG CAATGCACGT GGCCAGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGTTGTAA GGACTCACCT GAAATCTGGG CTCGGTTGC

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAACGGAGC CCAGATTCA GGTGAGTCCT TACAACCTC

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCTAGATAT CTCTAGACTA TAAATCTCTG GCCATGAAG

39

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

10027075.122001

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCACTAGGT CGACTCTAGA AACTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTAATC 60
TGGGCTCCGT TGC 73

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGAGAGAC ATATGGCAAT GCACGTGGCC CAGCCTGCTG TGG 43

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGAGAGAG GATCCTCAGT CAGTTAGTCA GAATCTGGGC ACGGTTCTGG 50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCAGCTAGTC ATGAAATACC TATTGCCTAC GGCAGCCGCT GGATTGTTAT TACTCGCTGC	60
CCAACCAGCG ATGGCCGCGAG CAATGCACGT GGGCCAGCCT GCTGTGG	107

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCTTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCGGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAAT CAAGTGAACC TACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTATG GTAATTGATC CAGAACCCTG CCCAGATTCT GATCAGGAGC CCAAATCTTC	600
TGACAAAAC TACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG	660
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCC CAGCGGGGTG	720
CTGACACGTC CACCTCCATC TCTTCTCAG CACCTGAAGC CGAGGGGGCA CCGTCAGTCT	780
TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT	840
GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG	900
GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC	960
GGGTGGTCAG CGTCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT	1020

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GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC AAAGCCAAAG 1080
 GTGGGACCCG TGGGGTGCGA GGGCCACATG GACAGAGGCC GGCTCGGCC ACCCTCTGCC 1140
 CTGAGAGTGA CCGCTGTACC AACCTCTGTC CTACAGGGCA GCGCCGAGAA CCACAGGTGT 1200
 ACACCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTGAGCCTG ACCTGCTGCG 1260
 TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGAGGA 1320
 ACAAATACAA GACCACGCTT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA 1380
 AGTCCACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC 1440
 ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGAG 1500
 TGGCAGCGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA TGCTTGGCAC 1560
 GTACCCCTGT TACATACTTC CCGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGCTGCCC 1620
 TGGGCCCCCTG CGAGACTGTG ATGGTTCTTT CCACGGGTCA GGCCGAGTCT GAGGCCTGAG 1680
 TGGCATGAGG GAGGCAGAGC GGGTC 1705

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
 20 25 30
 Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
 35 40 45
 Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
 50 55 60
 Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
 65 70 75 80
 Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
 85 90 95

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Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
130 135 140

Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
145 150 155 160

Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1747 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTGCTTA	CCTGAGAAG	CTTGAGATCA	CAGTTCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTACCA	TGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAGGCCAC	300
TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGGAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAAC	540
CCAGATTTAT	GTAATTGATC	CAGAACCCTG	CCCAGATTCT	GATCAGGAGT	CCAAATATGG	600
TCCCCATCC	CCATCATCCC	CAGGTAAGCC	AACCCAGGCC	TCGCCCTCCA	GCTCAAGGCG	660
GGACAGGTGC	CCTAGAGTAG	CCTGCATCCA	GGGACAGGCC	CCAGCCGGGT	GCTGACGCAT	720
CCACCTCCAT	CTCTTCCTCA	GCACCTGAGT	TCCTGGGGGG	ACCATCAGTC	TTCTGTGTCC	780
CCCCAAAACC	CAAGGACACT	CTCATGATCT	CCCGGACCCC	TGAGGTACAG	TGCGTGGTGG	840
TGGACGTGAG	CCAGGAAGAC	CCCGAGGTCC	AGTTCAACTG	GTACGTGGAT	GGCGTGGAGG	900
TGCATAATGC	CAAGACAAAG	CCGCGGGAGG	AGCAGTTCAA	CAGCACGTAC	CGTGTGGTCA	960
GCCTCTCAC	CGTCTGCAC	CAGGACTGGC	TGAACGGCAA	GGAGTACAAG	TGCAAGGTCT	1020
CCACAAAGG	CCTCCCGTCC	TCCATCGAGA	AAACCATCTC	CAAAGCCAAA	GGTGGGACCC	1080
ACGGGGTGCG	AGGGCCACAC	GGACAGAGGC	CAGCTCGGCC	CACCCCTCTG	CCTGGGAGTG	1140
ACCGCTGTGC	CAACCTCTGT	CCCTACAGGG	CAGCCCCGAG	AGCCACAGGT	GTACACCCCTG	1200
CCCCCATCCC	AGGAGGAGAT	GACCAAGAAC	CAGGTCAGCC	TGACCTGCCT	GGTCAAAGGC	1260
TTCTACCCCA	GCGACATCGC	CGTGGAGTGG	GAGAGCAATG	GGCAGCCGGA	GAACAACTAC	1320
AAGACCACGC	CTCCCGTGCT	GGACTCCGAC	GGCTCCTTCT	TCCTCTACAG	CAGGCTAACC	1380
GTGGACAAGA	GCAGGTGGCA	GGAGGGGAAT	GTCTTCTCAT	GCTCCGTGAT	GCATGAGGCT	1440

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CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG	1500
CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTGCGCGGA GGATGCTTGG CACGTACCCC	1560
GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAGCA CCCACCACTG CCCTGGGCCC	1620
CTGTGAGACT GTGATGGTTC TTTCCACGGG TCAGGCCGAG TCTGAGGCCT GAGTGACATG	1680
AGGGAGGCAG AGCGGTCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT	1740
CCTCTGC	1747

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	1	5	10	15
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser	20	25	30	
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys	35	40	45	
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val	50	55	60	
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe	65	70	75	80
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn	85	90	95	
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys	100	105	110	
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn		115	120	125	
Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	130	135	140	
Gln	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Ser	Pro	Ser	Ser	Pro	Ala	Pro	Glu	145	150	155	160
Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Pro	Pro	Lys	Pro	Lys	Asp		165	170	175	

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Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 180 185 190
 Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 195 200 205
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 210 215 220
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 225 230 235 240
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 245 250 255
 Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 260 265 270
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
 275 280 285
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 290 295 300
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 305 310 315 320
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
 325 330 335
 Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
 340 345 350
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 355 360 365
 Ser Leu Ser Leu Gly Lys
 370

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCTTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGAGA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTAT GTAATTGATC CAGAACCCTG CCCAGATTCT GATCAGGAGT CCAATATATG	600
TCCCCATCC CCATCATCCC CAGGTAAGCC AACCAGGCC TCGCCCTCCA GCTCAAGGCG	660
GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT	720
CCACCTCCAT CTCTTCCTCA GCACCTGAGT TCGAGGGGGC ACCATCAGTC TTCTGTTC	780
CCCCAAAACC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TCGTGGTGG	840
TGACAGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCCTGGAGG	900
TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTGGTCA	960
CGCTCTCACC CGTCTGACC CAGGACTGAC TGAACGGCAA GGAGTACAAG TGCAAGGTCT	1020
CCAACAAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGAGCC	1080
ACGGGGTGCG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCCTGTC CCTGGGAGTG	1140
ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCTTG	1200
CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC	1260
TTCTACCCCA GEGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACATC	1320
AAGACCACGC CTCCTGTGCT GGAATCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAACC	1380
GTGGACAAGA GCAGGTGGCA GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT	1440
CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG	1500
CCGGCAAGCC CCGCTCCCC GGGCTCTCGG GGTCCGCGGA GGATGCTTGG CACGTACCCC	1560
GTCTACATAC TTCCACGGCA CCCAGCATGG AAATAAAGCA CCCACCACTG CCCTGGGCCC	1620
CTGTGAGACT GTGATGGTTC TTCCACGGG TCAGGCCGAG TCTGAGGCCT GAGTGACATG	1680
AGGGAGGCAG AGCGGTCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT	1740

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1747

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
 20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
 35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
 50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
 65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
 85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
 100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
 115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
 130 135 140

Gln Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser Ser Pro Ala Pro Glu
 145 150 155 160

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 165 170 175

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 195 200 205

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Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 210 215 220
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 225 230 235 240
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 245 250 255
 Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 260 265 270
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
 275 280 285
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 290 295 300
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 305 310 315 320
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
 325 330 335
 Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
 340 345 350
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 355 360 365
 Ser Leu Ser Leu Gly Lys
 370

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTGCTTA CCTGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300

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TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGAGA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC	540
CCAGATTTC AAGTGAGTCT TACAACCTCT CTCTTCTATT CAGCTTAAAT AGATTITACT	600
GCATTGTGTG GGGGGGAAAT GTGTGTATCT GAATTTCAGG TCATGAAGGA CTAGGGACAC	660
CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG CAGACAGACA TCCTCAGCTC	720
CCAGACTTCA TGGCCAGAGA TTTATAGTCT AGAGGATCCC CAGCTTCTG GGGCAGGCCA	780
GGCCTGACCT TGGCTTTGGG GCAGGGAGGG GGCTAAGGTG AGGCAGGTGG CGCCAGCAGG	840
TGCACACCCA ATGCCCCATGA GCCCAGACAC TGGACGCTGA ACCTCGCGGA CAGTTAAGAA	900
CCCAGGGGCC TCTGCGCCTG GGCCAGCTC TGTCCCACAC CGCGGTCA CA TGCCACCACC	960
TCTCTGCGAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCTC TCCTCAAGAGC	1020
ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG	1080
ACGGTGTCTG GGAACCTCAG CGCCCTGACC AGCGCGCTGC ACACCTTCCC GGCTGTCTTA	1140
CAGTCTCTAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC	1200
ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA	1260
GTTGGTGAGA GGCACGACA GGGAGGGAGG GTGTCTGCTG GAAGCAGGCT CAGCGCTCCT	1320
GCCTGGAGCG ATCCCCGCTA TGCAGCCCCA GTCCAGGGCA GCAAGGCAGG CCCCCTCTGC	1380
CTCTTACACC GGAGCCTCTG CCGCCCCAC TCATGCTCAG GGAGAGGGTC TTCTGGCTTT	1440
TTCCAGGCT CTGGGCAGGC ACAGGCTAGG TGCCCTAAC CCAGGCCCTG CACACAAAGG	1500
GGCAGGTGCT GGGCTCAGAC CTGCCAAGAG CCATATCCGG GAGGACCTG CCCCTGACCT	1560
AAGCCCACCC CAAAGGCCAA ACTCTCCACT CCCTCAGCTC GGACACCTT TCTCTCTCCA	1620
GATTCCAGTA ACTCCCAATC TTCTCTCTGC AGAGCCCCAA TCTGTGACA AAATCTACAC	1680
ATGCCACCG TGCCCAAGTA AGCCAGCCCC GGCTCGCC TCCAGCTCAA GCGGGACAG	1740
GTGCCCTAGA GTAGCTGCA TCCAGGGACA GGGCCAGCC GGGTGTCTGAC ACGTCCACCT	1800
CCATCTCTTC CTCAGCACCT GAACTCCTGG GGGGACCGTC AGTCTCTCTC TTCCCCCA	1860
AACCAAGGA CACCTCATG ATCTCCCGGA CCCCTGAGGT CACATGCGTG GTGGTGACG	1920
TGAGCCACGA AGACCTGAG GTCAAGTTCA ACTGGTACGT GGACGGCGTG GAGGTGCATA	1980
ATGCCAAGAC AAAGCCCGG GAGGAGCAGT ACAACGACAC GTACCGGGTG GTCAGCGTCC	2040

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TCACCGTCTCT GCACCGAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA 2100
 AAGCCCTCCC AGCCCCCCTC GAGAAAAACA TCTCCAAGC CAAAGGTGGG ACCCGTGGGG 2160
 TGGGAGGGCC ACATGGACAG AGGCCGGCTC GGCCCCCCTC CTGCCCTGAG AGTGACCGCT 2220
 GTACCAACCT CTGTCTCTACA GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT 2280
 CCGGGGATGA GCTGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC 2340
 CCAGCGACAT CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA 2400
 CGCCTCCCGT GCTGAGACTCC GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA 2460
 AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA 2520
 ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCGGGGTAA ATGAGTGCGA CGGCCGGCAA 2580
 GCCCCGCTCC CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT 2640
 ACTTCCCGGG CGCCAGCATG GGAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA 2700
 CTGTGATGGT TCTTTCCACG GGTGAGGCCG AGTCTGAGGC CTGAGTGGCA TGAGGGAGGC 2760
 AGAGCGGGTC 2770

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
 20 25 30
 Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
 35 40 45
 Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
 50 55 60
 Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
 65 70 75 80
 Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
 85 90 95

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Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
 100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
 115 120 125

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1708 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCGGG GTGACAGTGC TTGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480

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CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC	540
CCAGATTAATA CGTGAGTAGA ATTTAAACTT TGCTTCTCA GTTCTAGAA GAATGGCTGC	600
AAAGAGCTCC AACAAAACAA TTTAGAACTT TATTAAGGAA TAGGGGGAAG CTAGGAAGAA	660
ACTCAAAACA TCAAGATTTT AAATACGCTT CTGGTCTCC TTGCTATAAT TATCTGGGAT	720
AAGCATGCTG TTTTCTGTCT GTCCCTAACA TGCCCTGTGA TTATCCGCAA ACAACACACC	780
CAAGGGCAGA ACTTTGTTAC TTAAACACCA TCCGTGTTGC TTCTTTCTCTC AGGAACTGTG	840
GCTGCACCAT CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAAGTACC	900
TCTGTGTGTG GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA GTGGAAGGTG	960
GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA CAGAGCAGGA CAGCAAGGAC	1020
AGCACCTACA GCCTCAGCAG CACCTGACG CTGAGCAAAG CAGACTACGA GAAACACAAA	1080
GTCTACGCCT GCGAAGTCAC CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC	1140
AGGGGAGAGT GTTAGAGGGA GAAGTGCCCC CACCTGCTCC TCAGTTCCAG CCTGACCCCC	1200
TCCCACCTT TGCGCTCTGA CCCTTTTCC ACAGGGGACC TACCCCTATT GCGGTCTCTC	1260
AGCTCATCTT TCACCTCACC CCCCTCTCC TCCTTGCTT TAATTATGCT AATGTTGGAG	1320
GAGAATGAAT AAATAAAGTG AATCTTTGCA CCTGTGGTTT CTCTCTTCC TCAATTTAAT	1380
AATTATTATC TGTGTTTAC CAACTACTCA ATTTCTCTTA TAAGGGACTA AATATGTAGT	1440
CATCCTAAGG CGCATAACCA TTTATAAAAA TCATCCTTCA TTCTATTTTA CCCTATCATC	1500
CTCTGCAAGA CAGTCTCTCC TCAAACCCAC AAGCCTTCTG TCCTCACAGT CCCCTGGGCC	1560
GTGGTAGGAG AGACTTGCTT CCTTGTTTTC CCCTCCTCAG CAAGCCCTCA TAGTCCTTTT	1620
TAAGGGTGAC AGGTCTTACG GTCATATATC CTTTGATTCA ATTCCTGGG AATCAACCAA	1680
GGCAAAATTTT TCAAAAGAAG AAACCTGC	1708

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

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1	5	10	15
Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser			
20		25	30
Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys			
35	40	45	
Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val			
50	55	60	
Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe			
65	70	75	80
Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn			
85	90	95	
Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys			
100	105	110	
Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn			
115	120	125	
Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro			
130	135	140	
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu			
145	150	155	160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn			
165	170	175	
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser			
180	185	190	
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala			
195	200	205	
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly			
210	215	220	
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	

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